

FIG. 1

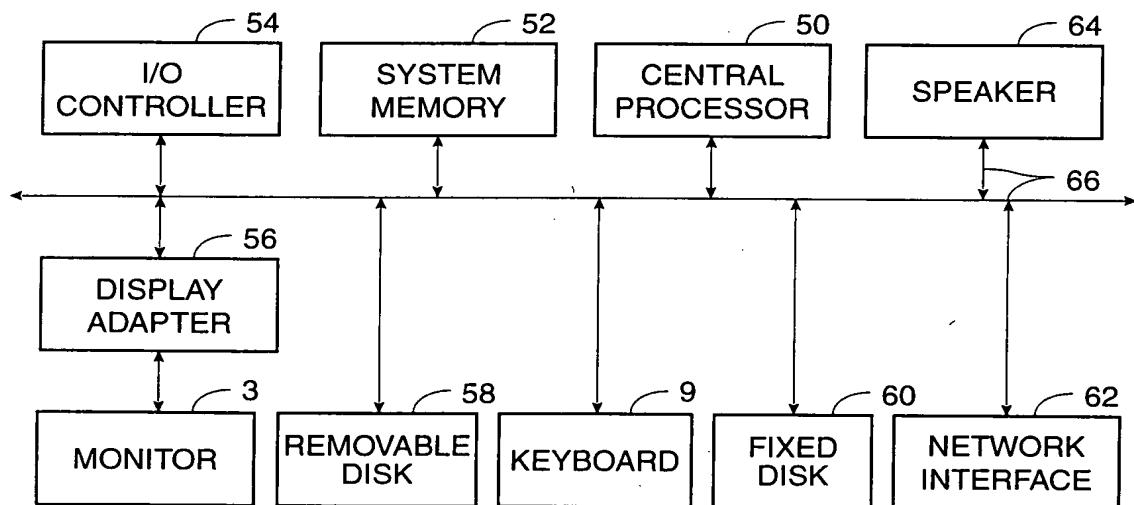


FIG. 2

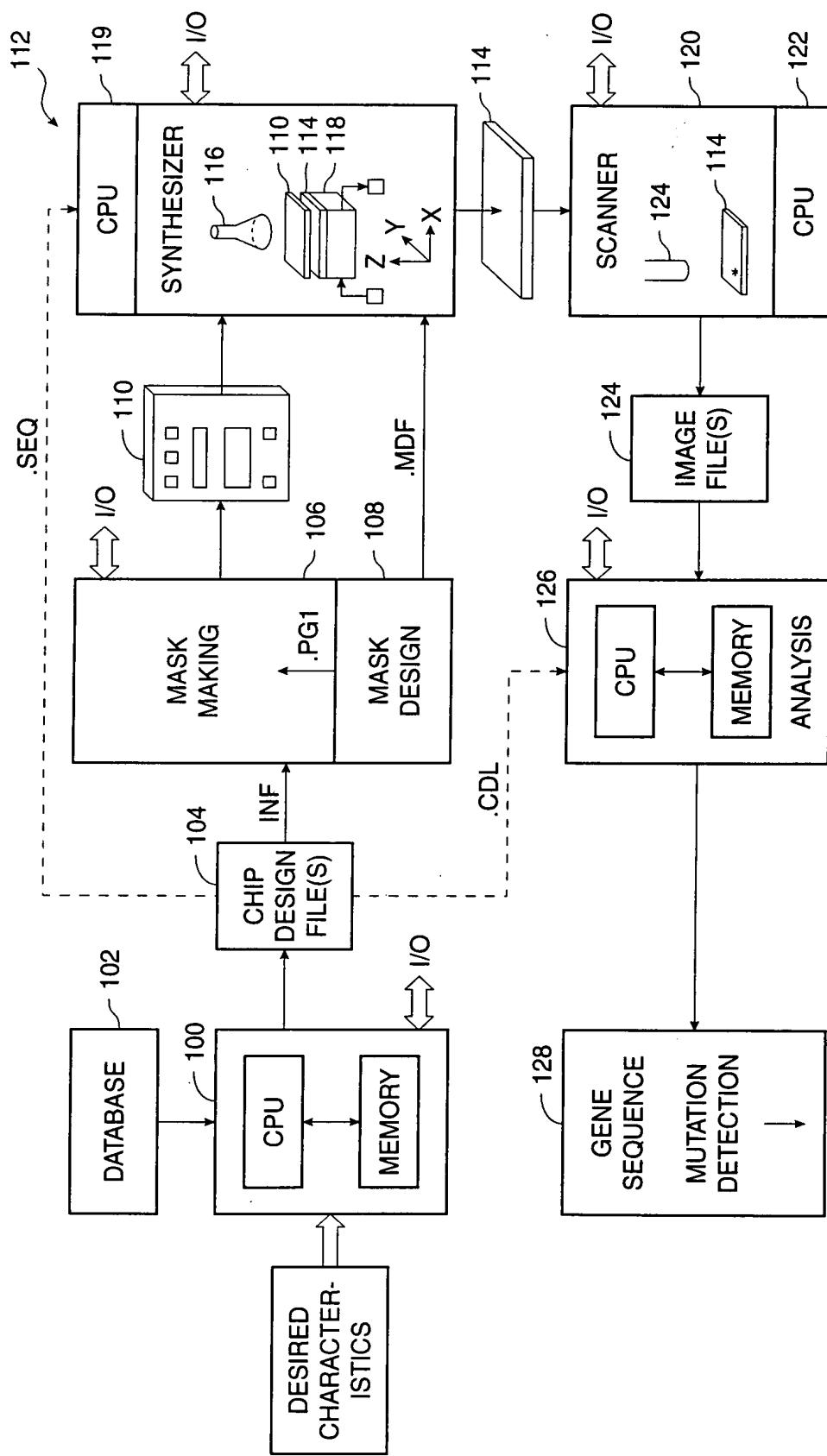


FIG. 3

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN	435	6

3/6

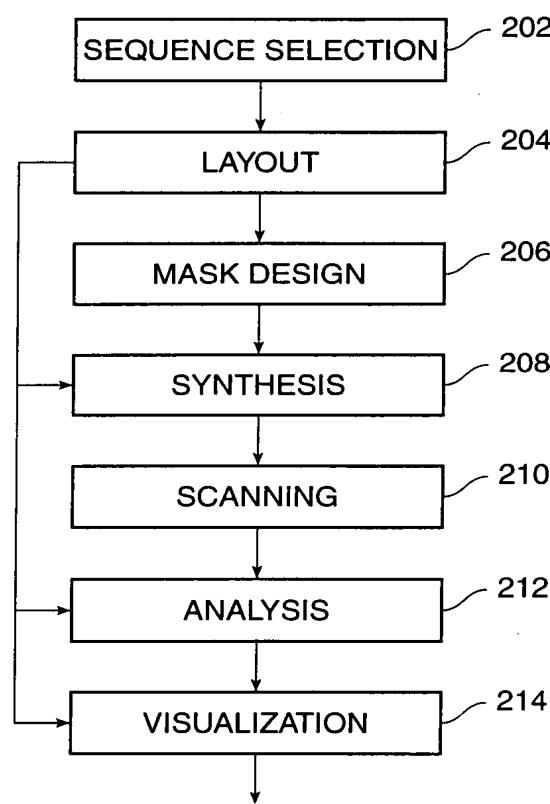


FIG. 4

APPROVED	O.G. FIG.
BY	
DRAFTSMAN	635 6

4/6

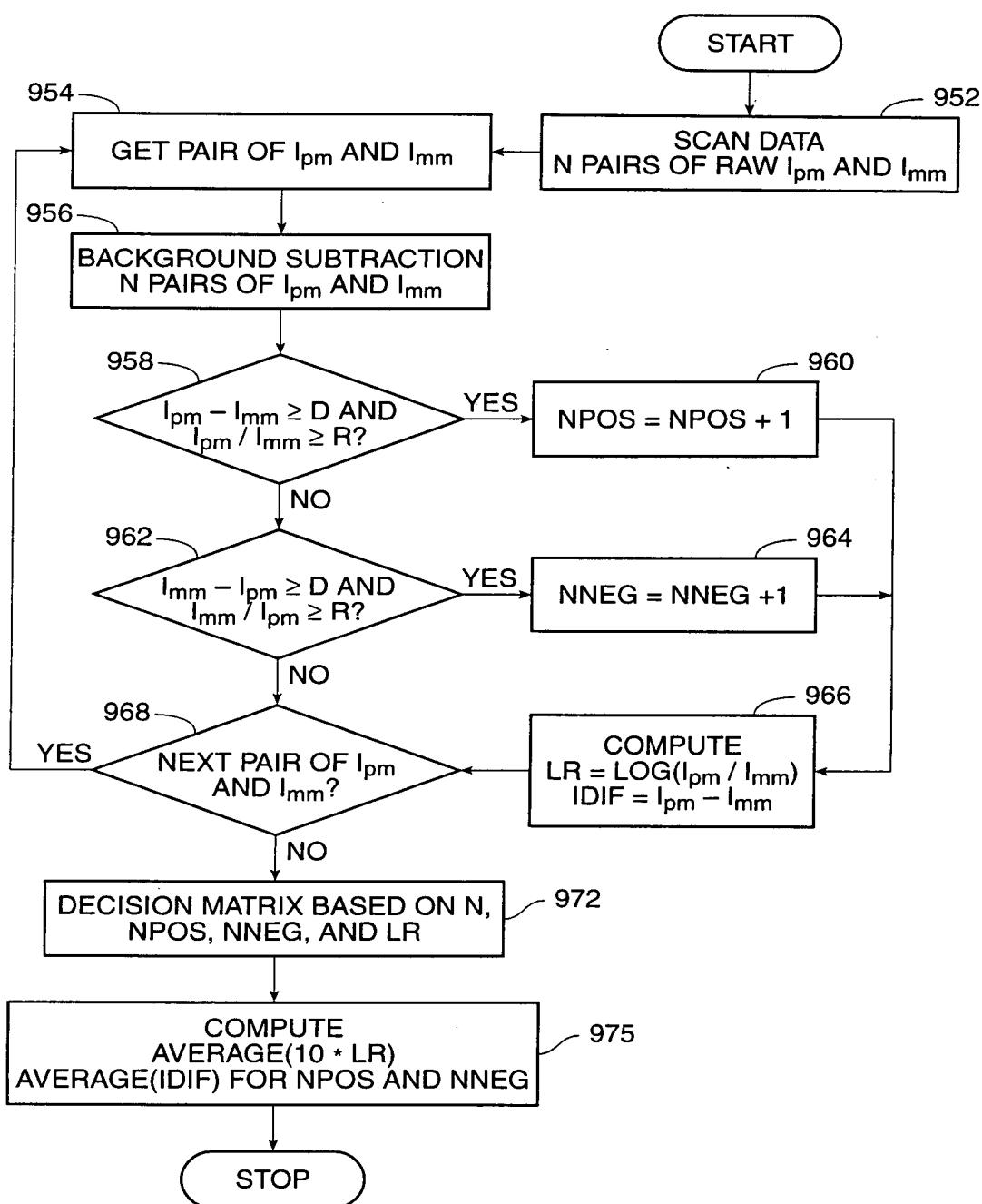


FIG. 5

APPROVED	O.G. FIG.
BY	
DRAFTSMAN	935
CLASS	SUBCLASS
	6

5/6

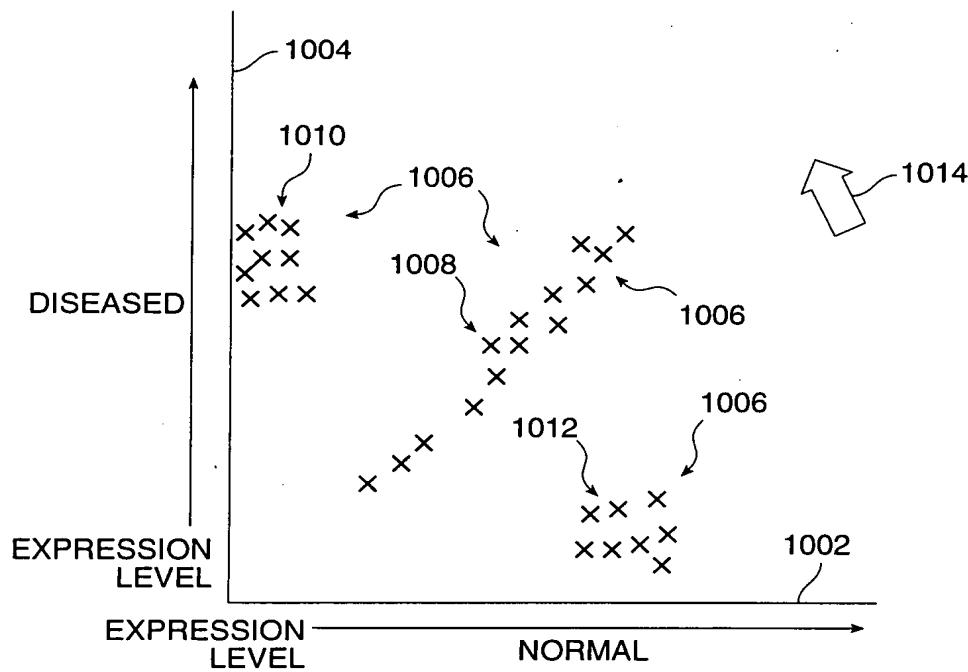


FIG. 6

CLUSTER	ACCESSION NUMBER	DESCRIPTION
Hsa.35 702	D11327 704	Human mRNA for protein-tyrosine phosphatase; complete cds. 706

FIG. 7A

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN	835	6

6/6

[http://www.ncbi.nlm.nih.gov/irx/cgi-bin/birx\\_doc?genbank+68169](http://www.ncbi.nlm.nih.gov/irx/cgi-bin/birx_doc?genbank+68169)

**LOCUS** HUMLCPTP 2691 bp mRNA **PRI** 06-NOV-1992  
**DEFINITION** Human mRNA for protein-tyrosine phosphatase, complete cds.  
**ACCESSION** D11327  
**NID** g219901  
**KEYWORDS** protein-tyrosine phosphatase.  
**SOURCE** Human T cell, lambda-gt10 library, cDNA to mRNA.  
**ORGANISM** Homo sapiens  
Eukaryote; mitochondrial eukaryotes; Metazoa; Chordata;  
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;  
Homo.  
**REFERENCE** 1 (bases 1 to 2691)  
**AUTHORS** Adachi,T., Sekiya,M., Isobe,M., Kumura,Y., Ogita,Z., Hinoda,Y.,  
Imai,K. and Yachi,A.  
**TITLE** Molecular cloning and chromosomal mapping of a human  
protein-tyrosine phosphatase LC-PTP  
**JOURNAL** Biochemical and Biophysical Research Communication 186, 1607-1615  
(1992)  
**COMMENT** Submitted (22-MAY-1992) to DDBJ by:  
Masaaki Adachi  
Sapporo Medical College  
S1W16 Chuo-ku  
Sapporo 060  
Japan  
Phone: 011-611-2111  
Fax: 011-613-1141.  
**FEATURES**  
**source** Location/Qualifiers  
1..2691  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/cell\_type="T cell"  
/clone\_lib="lambda-gt10  
**gene** 105..1187  
/gene="LC-PTP"  
**CDS** 105..1187  
/gene="LC-PTP"  
/codon\_start=1  
/product="protein-tyrosine phosphatase"  
/db\_xref="PID:d1002425"  
/db\_xref="PID:g219902"  
/translation="MVQAHGGRSRAQPLTLSLGAAMTQPPPEKTPAKKHVRLQERRGS  
NVALMLDVRSLGAVEPICSVNTPREVTLHFLRTAGHPLTRWALQRQPPSPKQLEEEFL  
KIPSNFVSPEDLDIPGHASKDRYKTILPNPQSRVCLGRAQSQEDGDYINANYIRGYDG  
KEKVIATQGPMPTNTVSDFWEMWQEEVSLIVMLTQLREGKEKCVHYWPTEETYGPF  
QIRIQDMKECPETYVRQLTIQYQEERRSVKHILFSAWPDHQTPESAGPLLRLVAEVEE  
SPETAAHPGPIVVHCSAGIGRTGCFIATRIGCQQLKARGEVDILGIVCQLRLDRGGMI  
QTDEQYQFLHHTLALYAGQLPEEPSP"  
**misc\_feature** 444..1172  
/gene="LC-PTP"  
/note="single catalytic domain"  
**polyA\_signal** 2667..2672  
**polyA\_site** 2691  
**BASE COUNT** 652 a 816 c 707 g 516 t  
**ORIGIN**  
1 ggagacagac agacagctgg caagaggcag cctgggggcc acagctgctt cagcagacct  
61 catggctgag tgaggctccc ctggggccag caccacccact cagcatggtc caagcccatg  
121 gggggcgtc cagagcacag ccgttgcaccc tgcgtttggg ggcagccatg acccagccctc  
181 cgcctgaaaa aacgcgcagc aagaagcatg tgccactgca ggagaggcgg ggctccaaatg  
241 tggctctgtat gctggacgtt cggccctgg gggccgtaga accccatctgc tctgtgaaca  
301 caccggggaa ggtcacccta cactttctgc gcactgctgg acacccctt acccgctgg  
361 cccttcagcg ccagccaccc agcccccaagc aactgaaaga agaattctt aagatccctt  
421 caaactttgt cagccccgaa gacctggaca tccctggcca cgcctccaaag gaccgataca  
481 agaccatctt gccaaatccc cagagccgtg tctgtctagg cccggcacaag agccaggagg...

**FIG. 7B**